Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Original) Method for neuroblastoma prognosis in a patient suffering from neuroblastoma, characterized in that it comprises the following steps:

a. biological material is extracted from a biological sample taken from the patient,

b. the biological material is brought into contact with at least one specific reagent chosen from the reagents specific for the target genes exhibiting a nucleic acid sequence having any one of SEQ ID Nos. 1 to 37, it being understood that, when the target gene exhibits a nucleic acid sequence having one of SEQ ID Nos. 11, 17 or 37, the biological material is brought into contact with at least two specific reagents chosen from the reagents specific for the target genes exhibiting a nucleic acid sequence having any one of SEQ ID Nos. 1 to 37,

c. the expression of at least one of said target genes is determined, it being understood that, when the target gene exhibits a nucleic acid sequence having one of SEQ ID Nos.11, 17 or 37, the expression of at least two of said target genes is determined.

2. (Original) Method for neuroblastoma prognosis according to Claim 1, characterized in that the biological sample taken from the patient is a tissue sample.

3. (Currently Amended) Method according to Claim 1 ~~or 2~~, characterized in that the biological material extracted during step a) comprises nucleic acids.

4. (Original) Method according to Claim 3, characterized in that the at least one specific reagent of step b) comprises at least one hybridization probe.

5. (Original) Method according to Claim 4, characterized in that the at least one hybridization probe is immobilized on a support.

6. (Original) Method according to Claim 5, characterized in that the support is a biochip.

7. (Currently Amended) Method according to ~~any one of Claims 1 to 6~~Claim 1, characterized in that, during step b), the biological material is brought into contact with at least 37 specific reagents chosen from the reagents specific for the target genes exhibiting a nucleic acid sequence having any one of SEQ ID Nos.1 to 37, and, during step c, the expression of at least 37 of said target genes is determined.

8. (Currently Amended) Method according to ~~any one of Claims 1 to 6~~Claim 1, characterized in that, during step b), the biological material is brought into contact with at least 19 specific reagents chosen from the reagents specific for the target genes exhibiting a nucleic acid sequence having SEQ ID No.1; SEQ ID No.2; SEQ ID No.3; SEQ ID No.7; SEQ ID No.8; SEQ ID No.9; SEQ ID No.10; SEQ ID No.14; SEQ ID No.16; SEQ ID No.20; SEQ ID No.21; SEQ ID No.22; SEQ ID No.25; SEQ ID No.27; SEQ ID No.29; SEQ ID No.31; SEQ ID No.34; SEQ ID No.36 or SEQ ID No.37, and, during step c), the expression of at least 19 of said target genes is determined.

9. (Currently Amended) Method according to ~~any one of Claims 1 to 6~~Claim 1, characterized in that, during step b), the biological material is brought into contact with at least 9 specific reagents chosen from the reagents specific for the target genes exhibiting a nucleic acid sequence having SEQ ID No.2; SEQ ID No.3; SEQ ID No.7; SEQ ID No.8; SEQ ID No.10; SEQ ID No.22; SEQ ID No.25; SEQ ID No.29; SEQ ID No.34 or SEQ ID No.37, and, during step c), the expression of at least 9 of said target genes is determined.